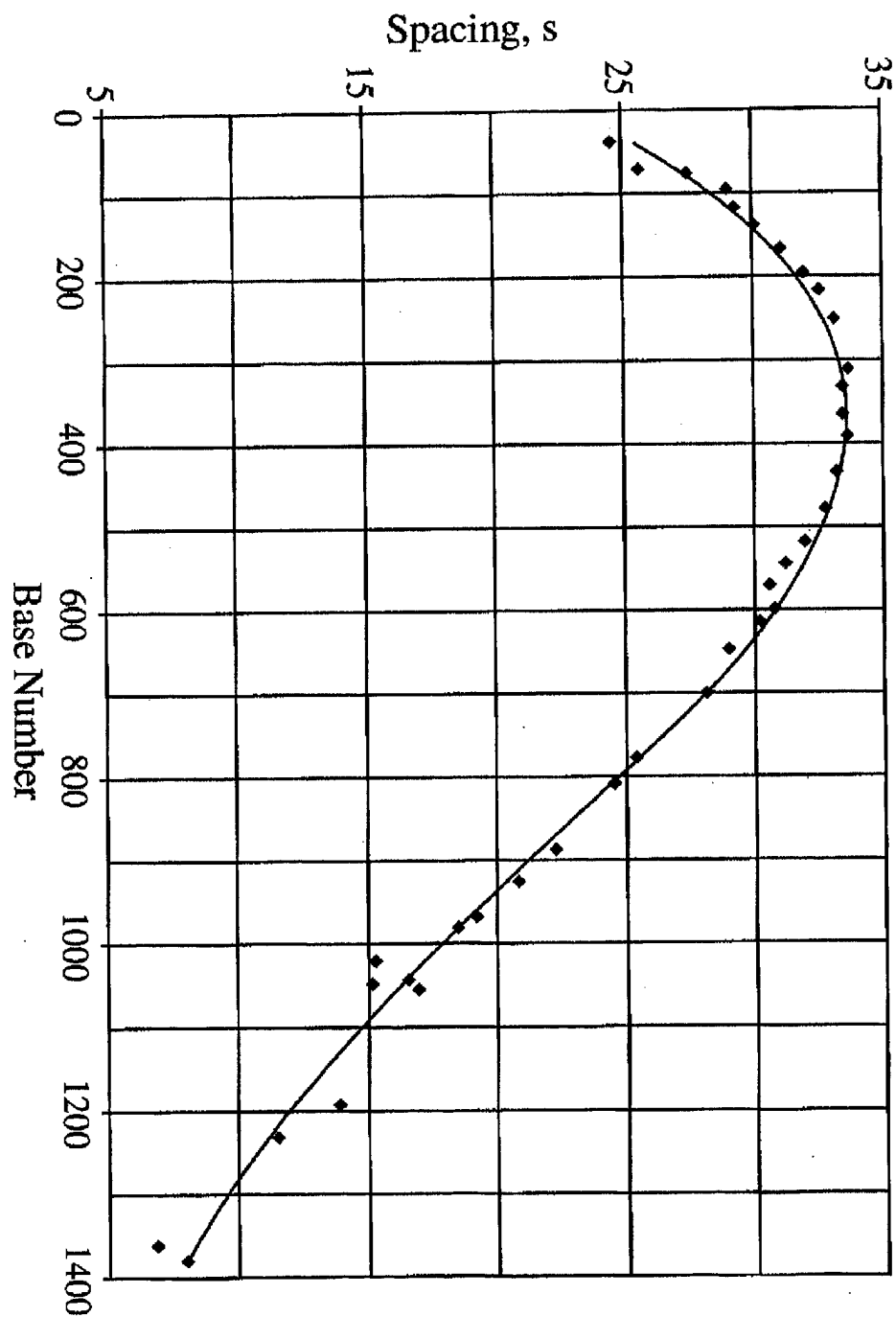Spacing Between Adjacent Peaks in the Raw Data
(M13, T's T=6% 60C, Long Gel)

FIG. 1

Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data
(M13, Long Gel, 55C, T=6%)
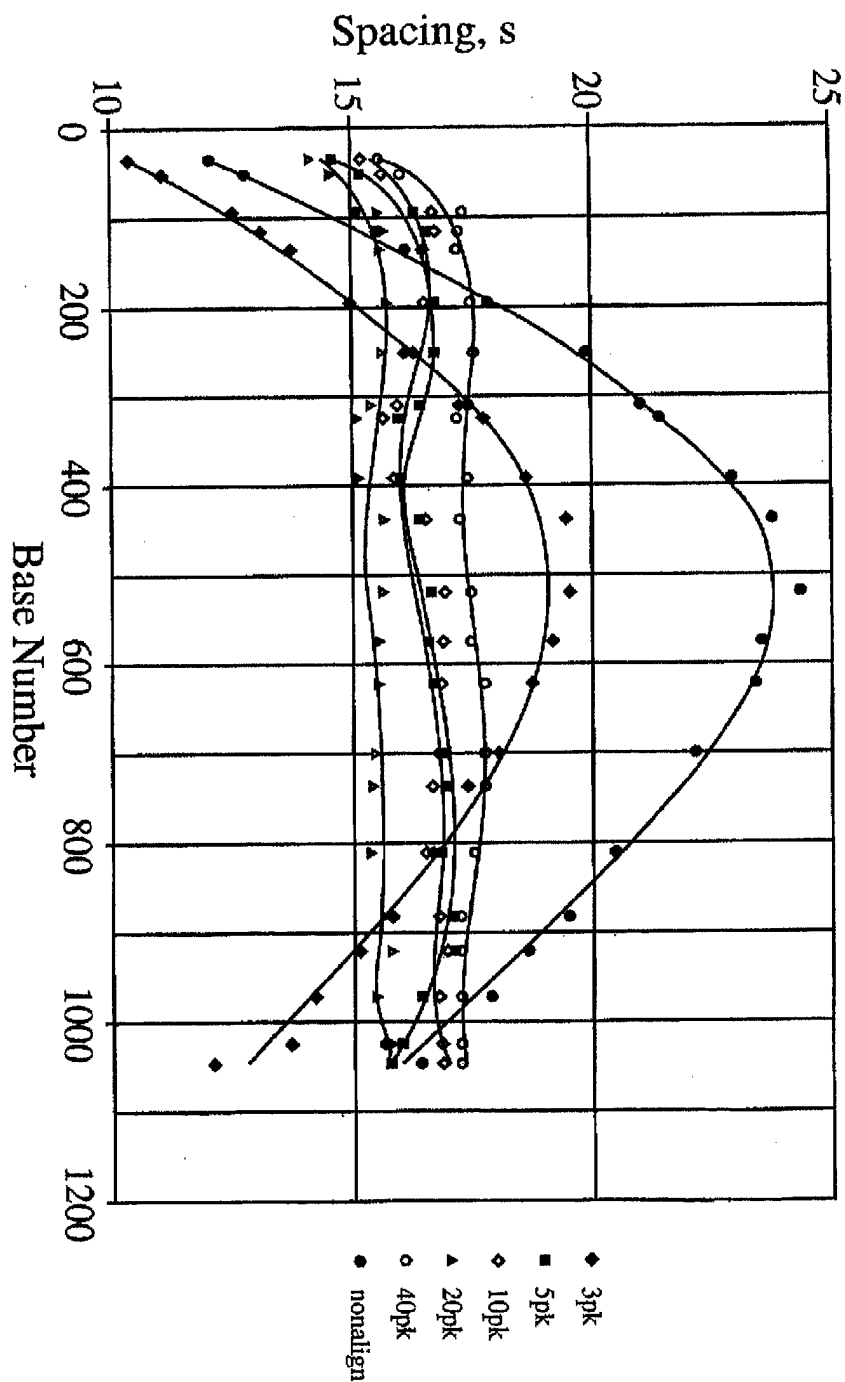
FIG. 2

Standard Deviation (%) of the Spacing Between Adjacent Bases from
Average as a Function of Number of Peaks Used as a Reference for
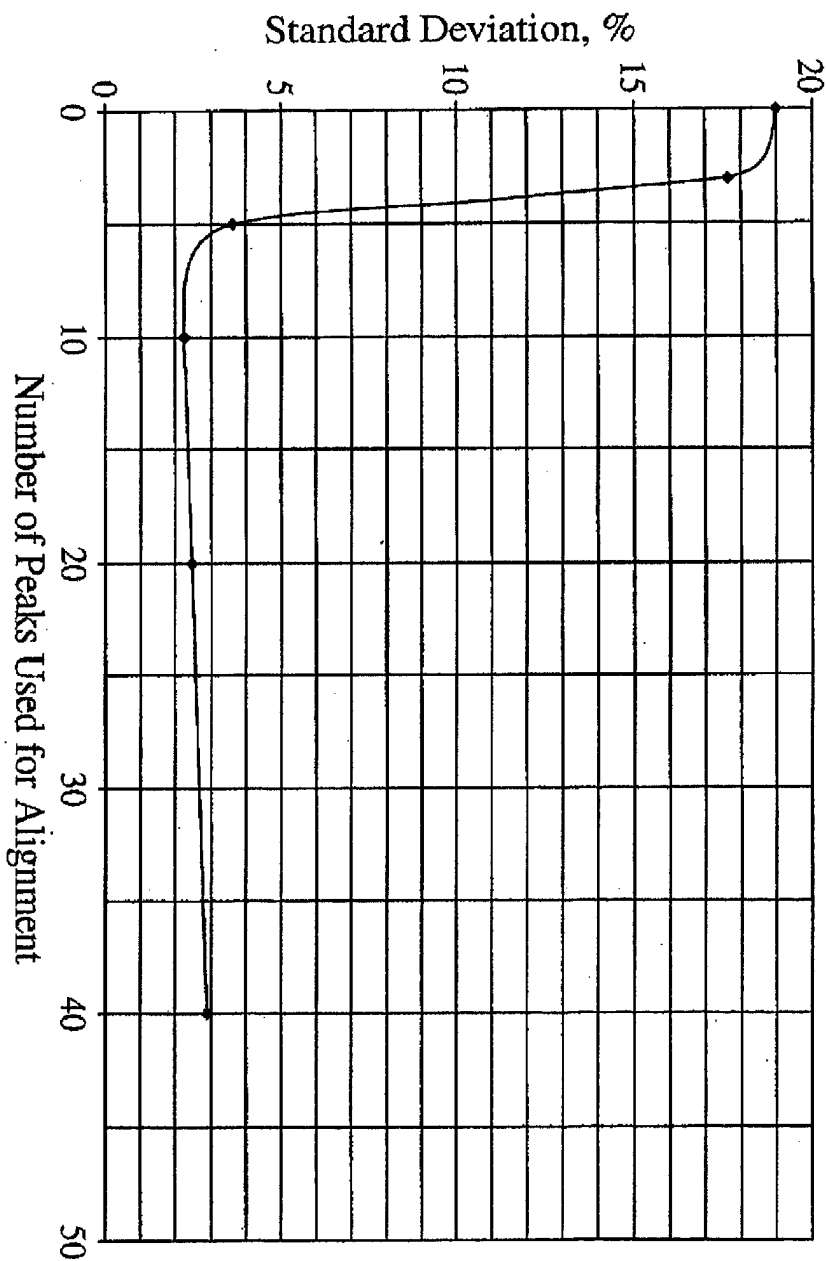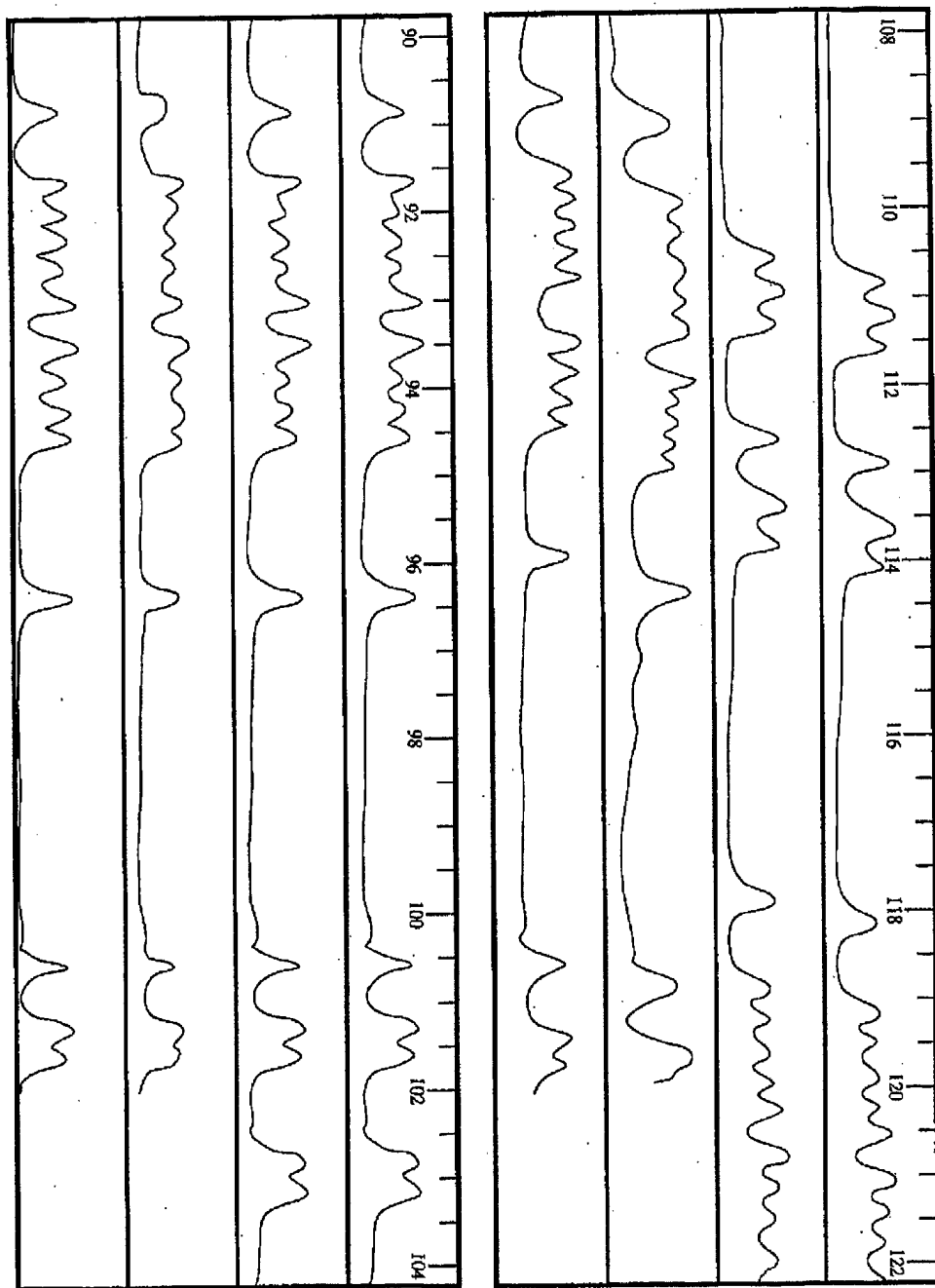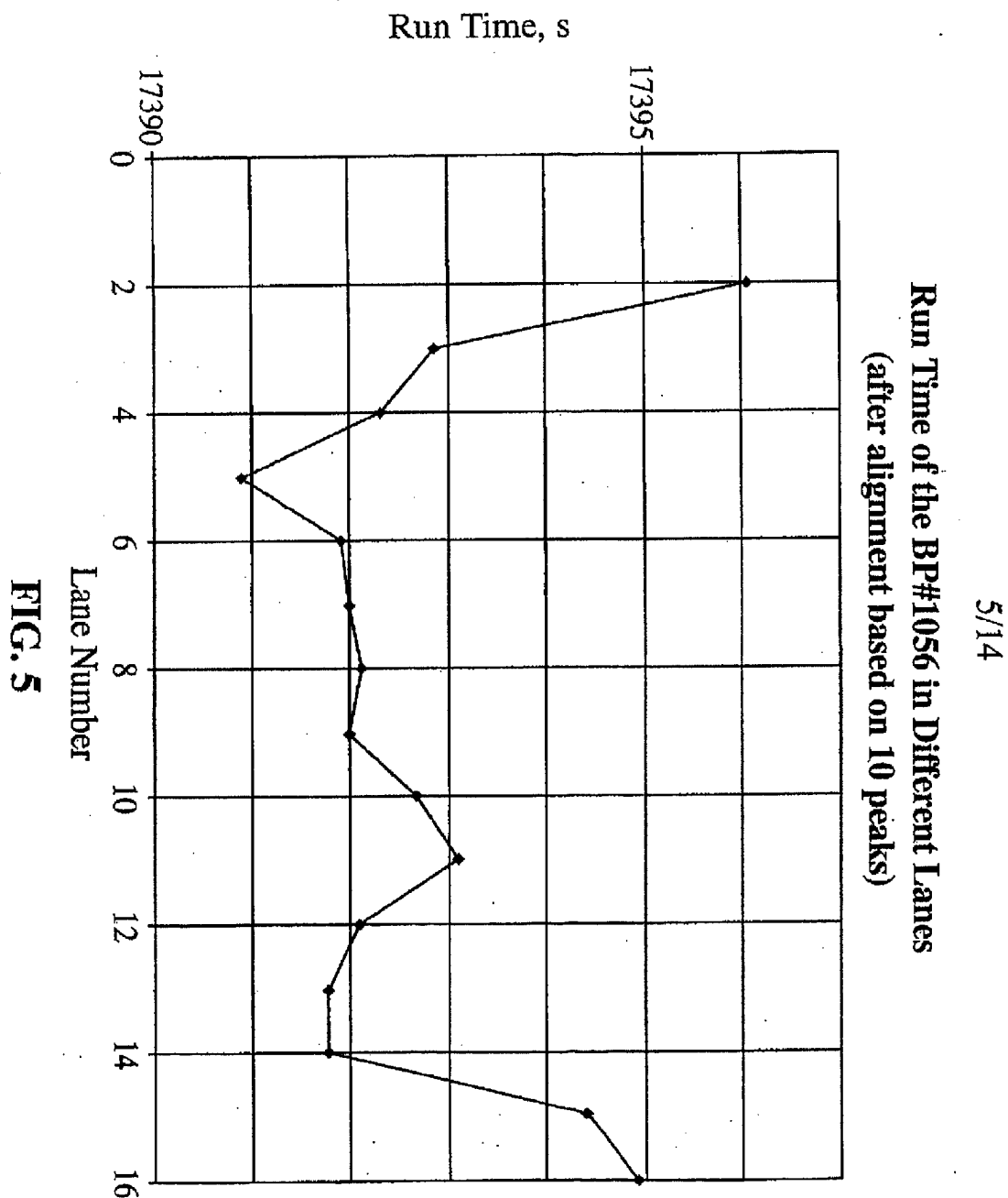Alignment of Raw Data

FIG. 3

FIG. 4

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Run Time of the BP#1056 in Different Lanes
(after alignment based on 10 peaks)

Run Time, s

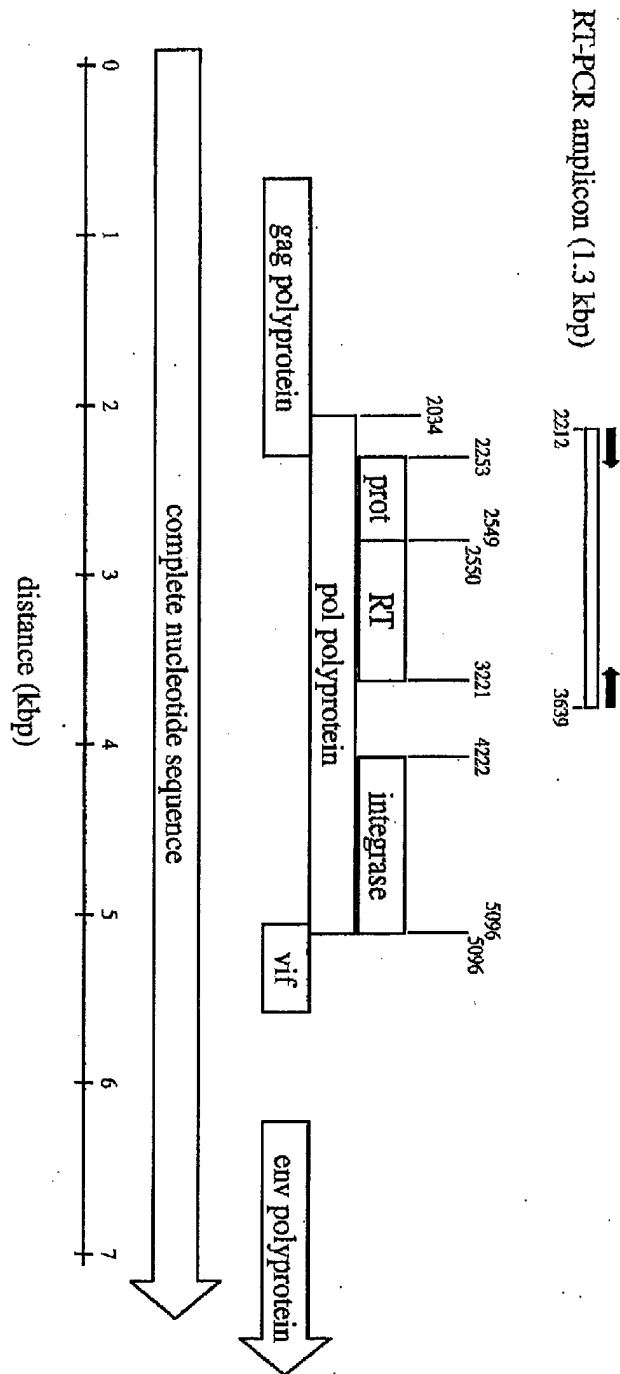FIG. 5

Lane Number

HIV-1 TruGene Kit (version 0.80)

FIG. 6

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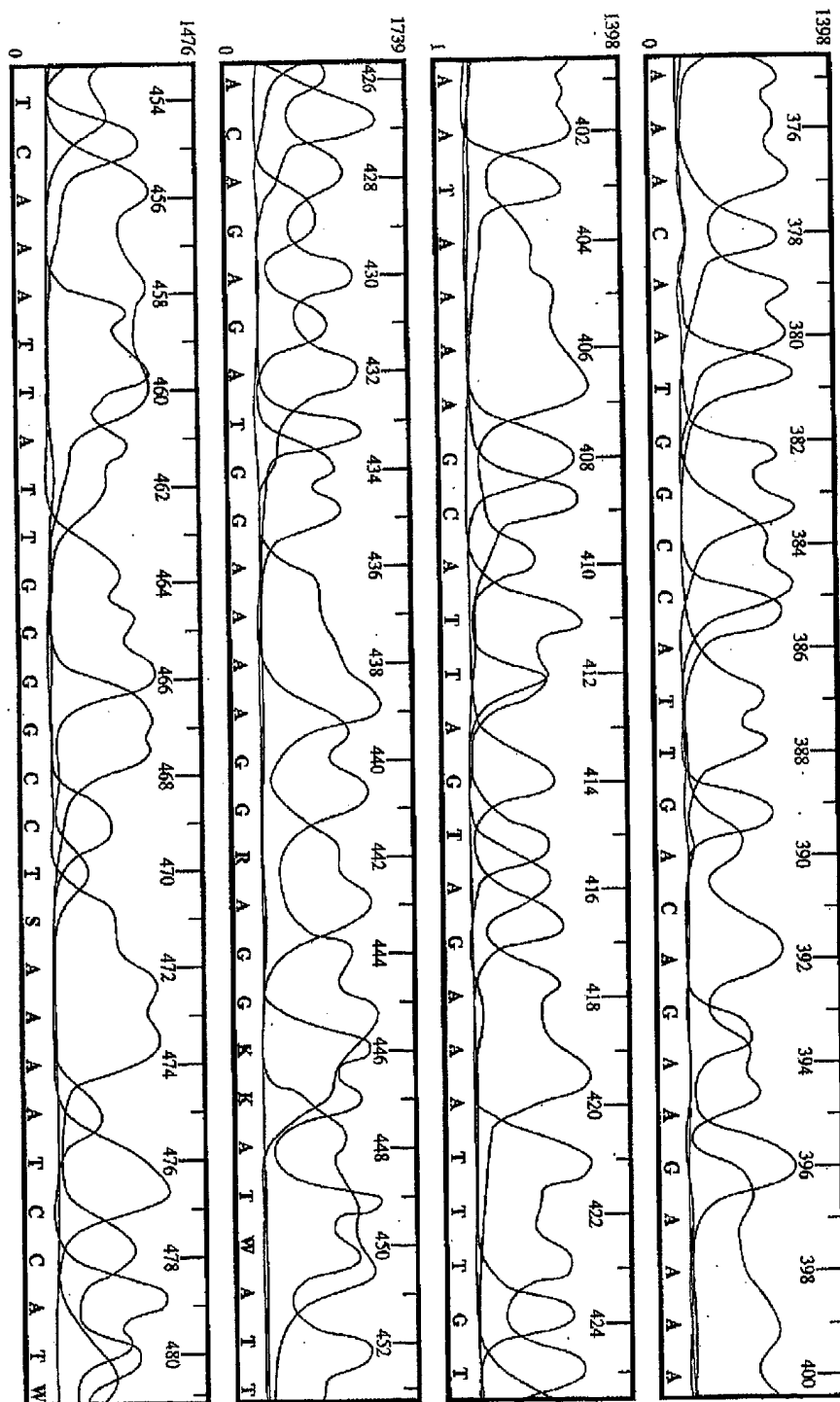Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

FIG. 7

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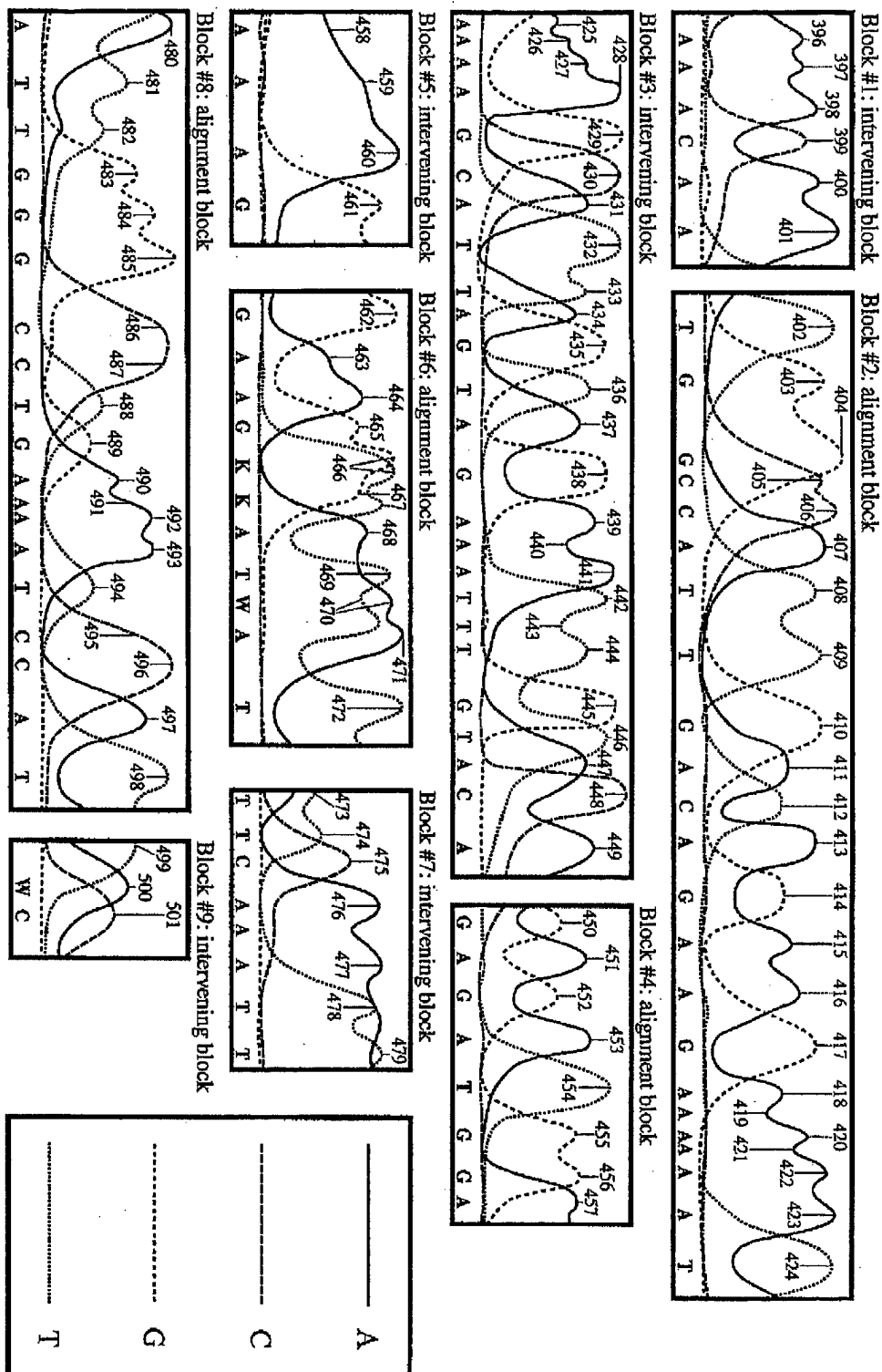# Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

FIG. 8

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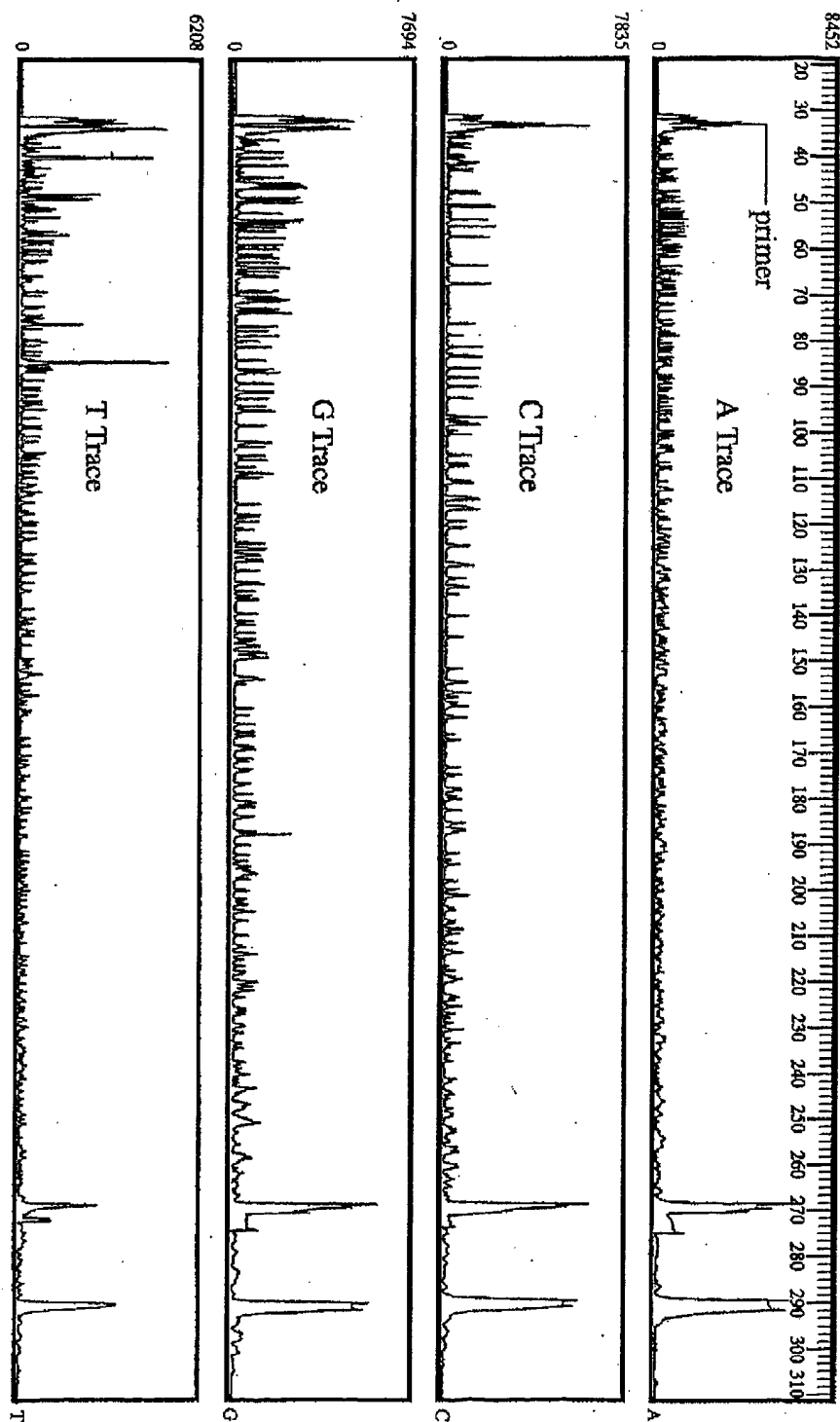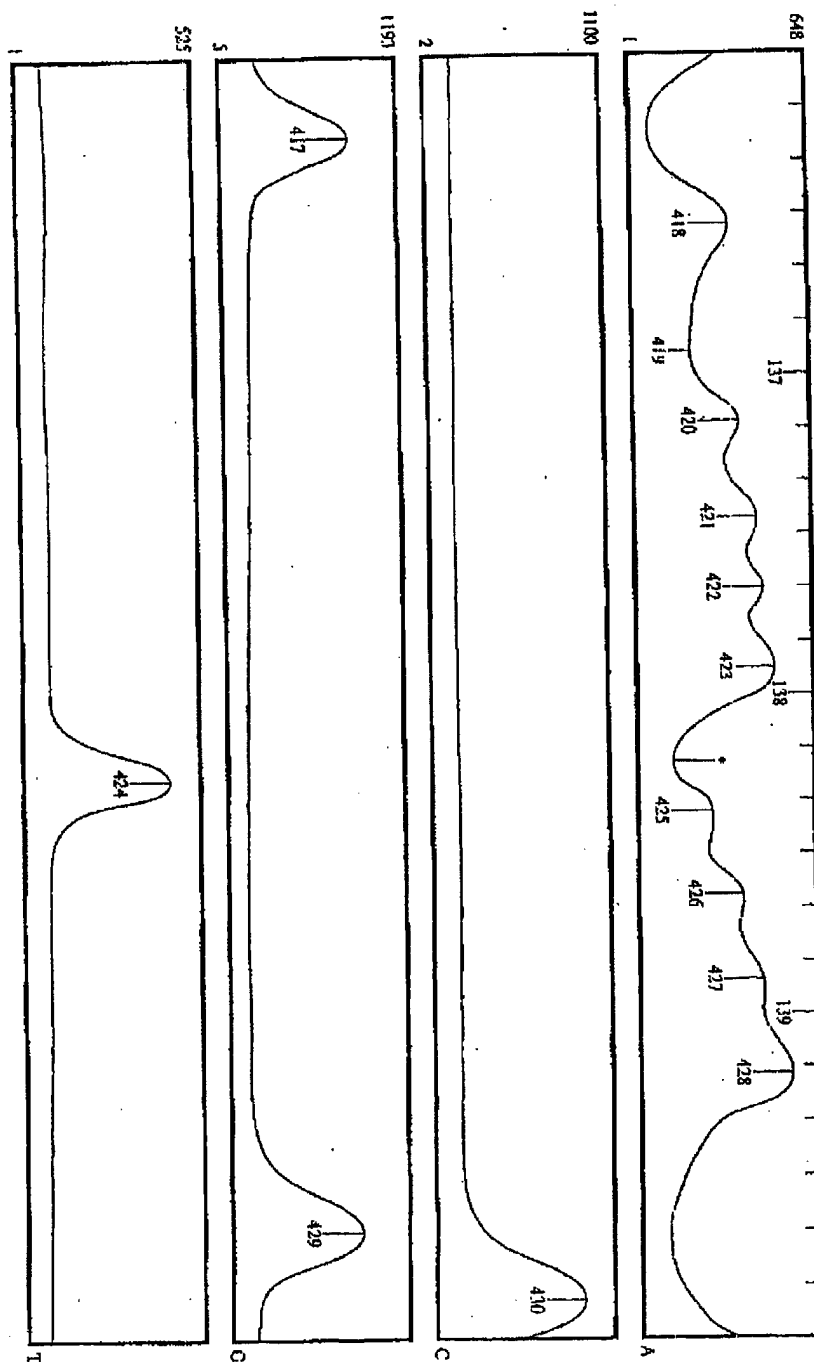Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

FIG. 9A

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FIG. 9B

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Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

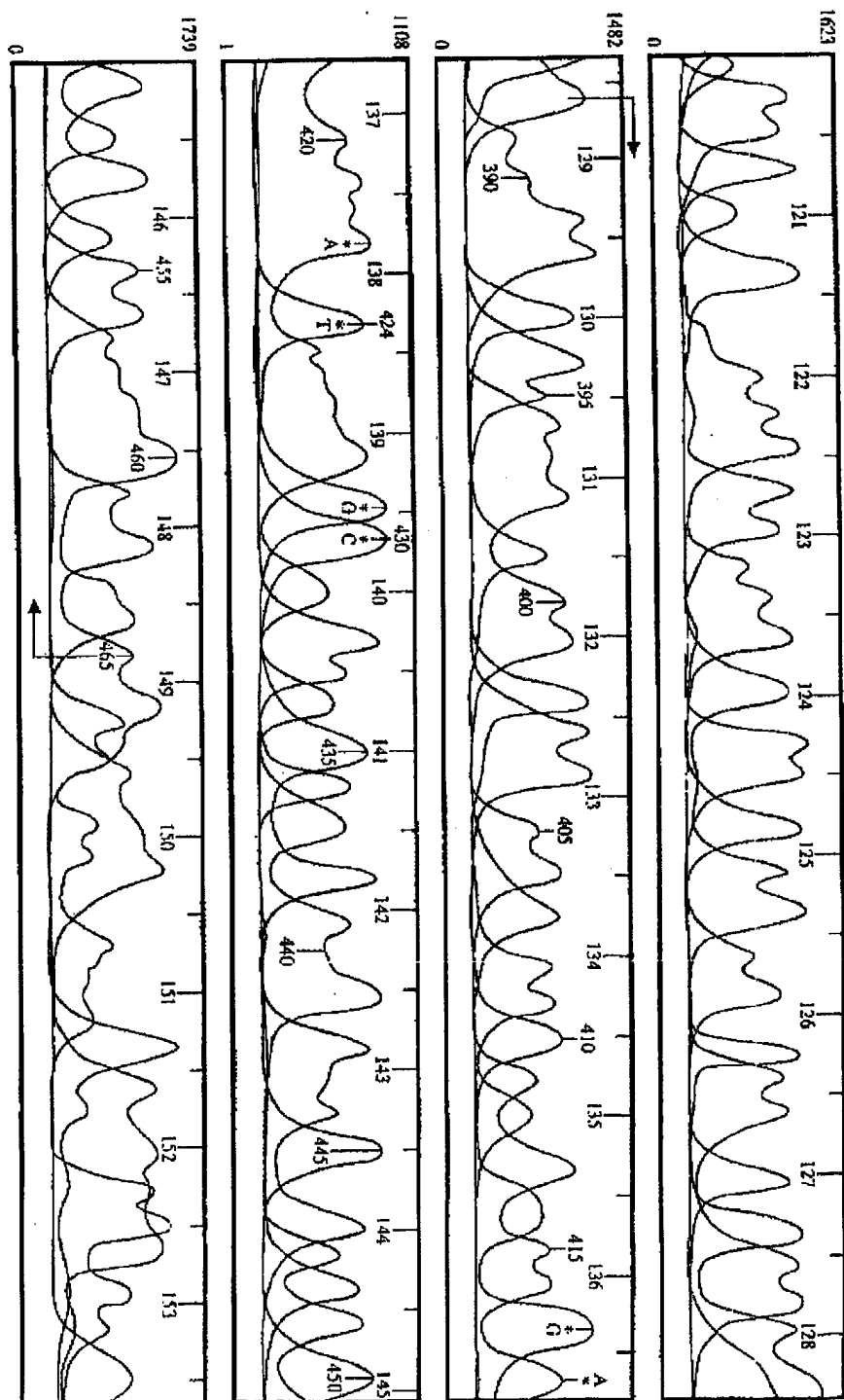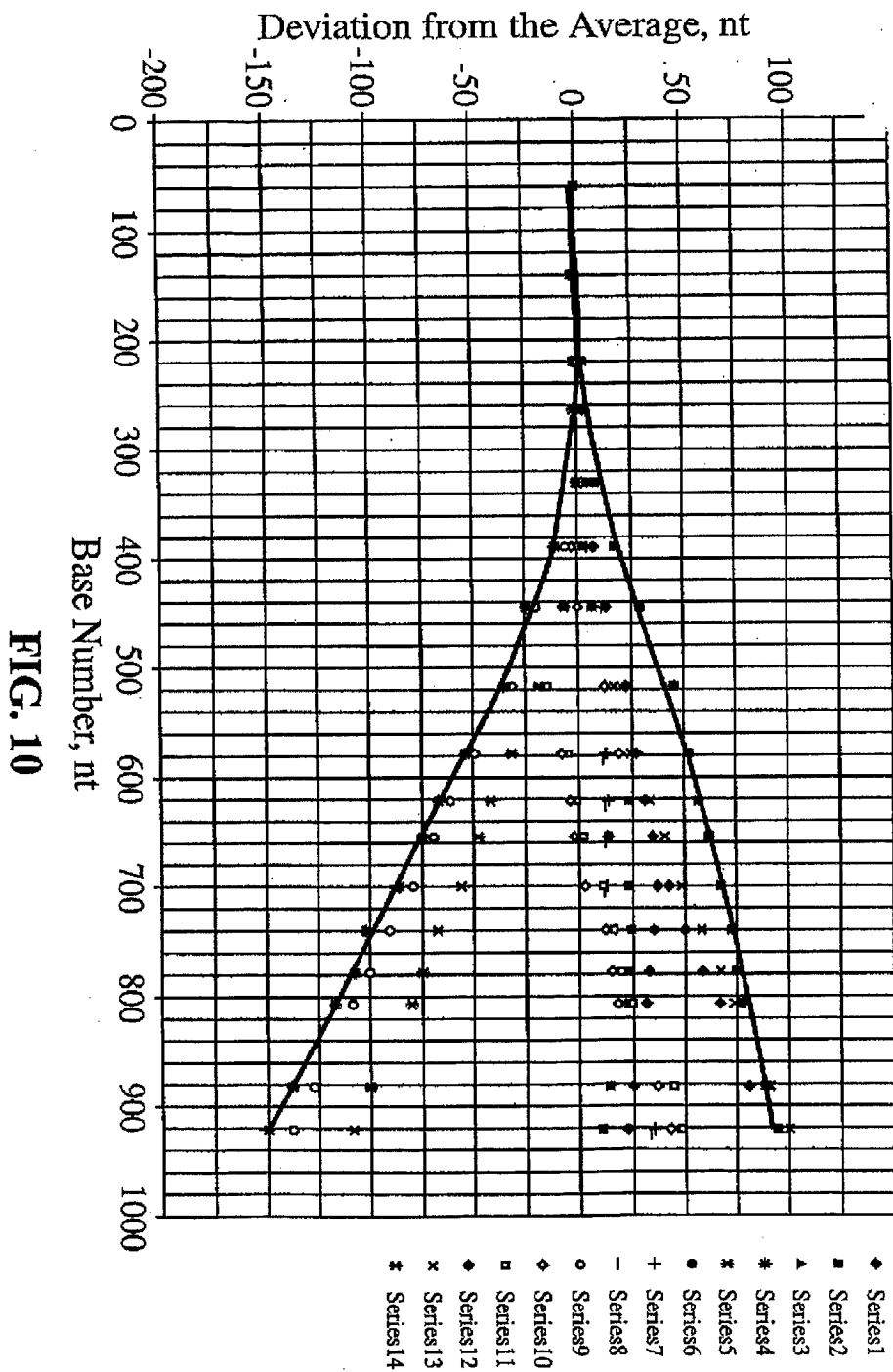FIG. 9C

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Deviation of the Peak Position (in Number of Bases) from the Average
as a Function of Base Number in Different Traces Before Alignment

FIG. 10

Deviation of the Peak Position (in Number of Bases) from the Average
as a Function of Base Number in the Traces Aligned with Internal Standards
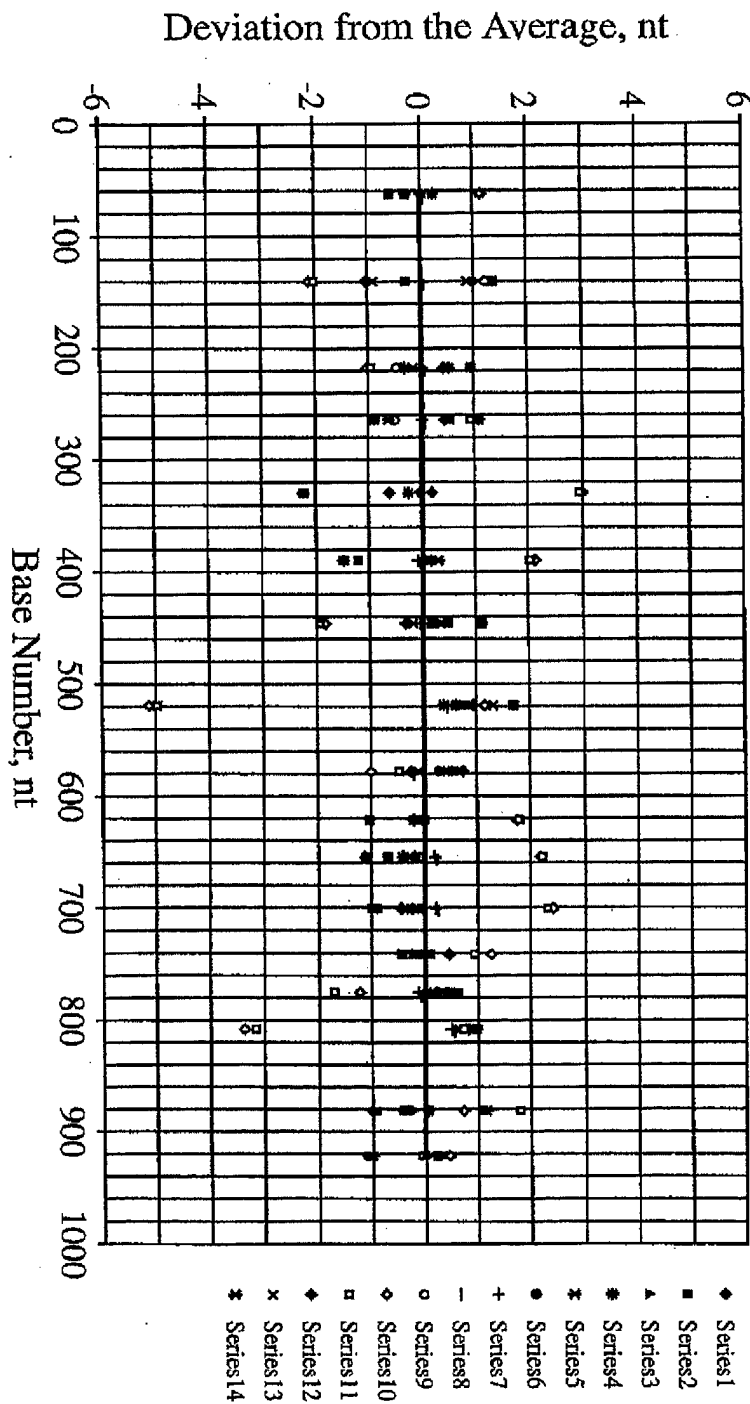(long gel, M13, 17 peaks, 5-th degree polynomial)

FIG. 11

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Deviation of the Peak Position from the Average as a Function
of Base Number in the Traces Aligned with Internal Standards
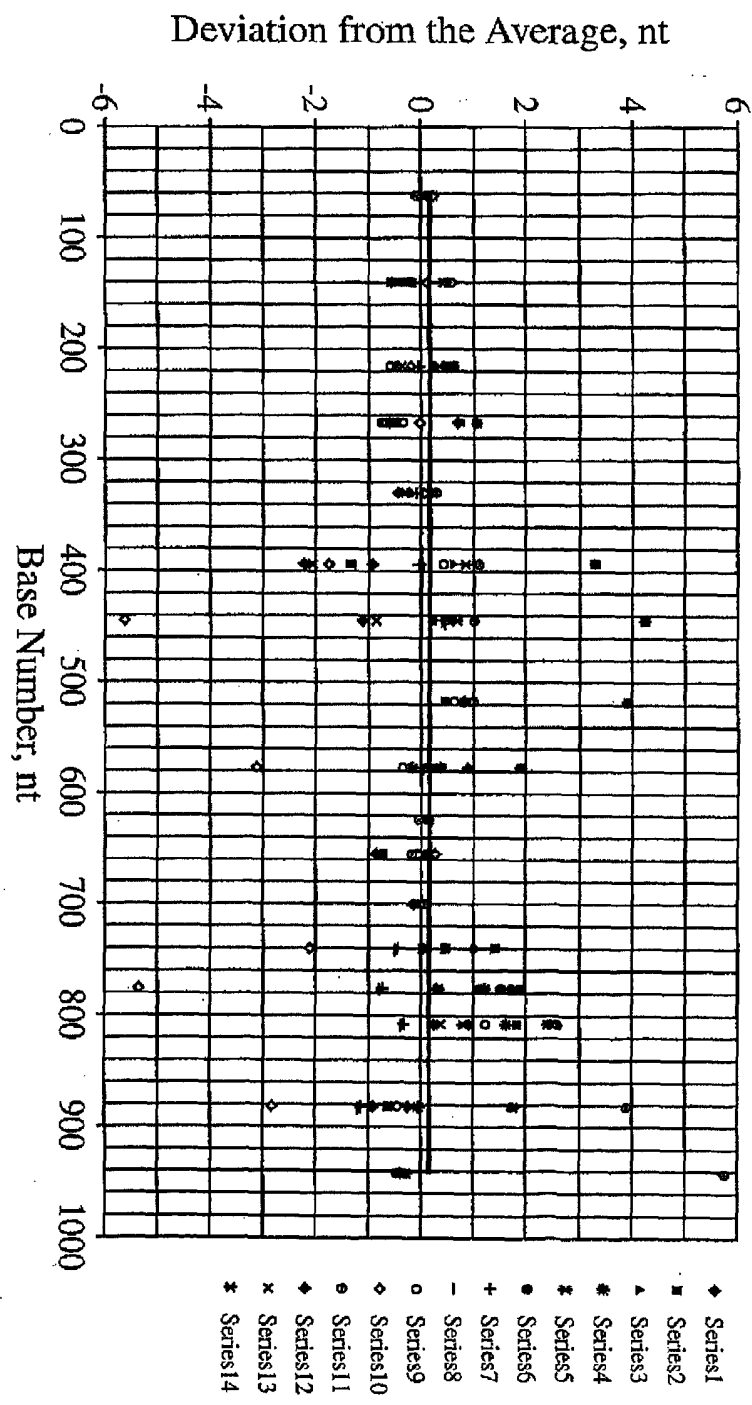(long gel, M13, 6 peaks, 5-th degree polynomial)

FIG. 12